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OM protein - protein search, using sw model

Run on: January 3, 2003, 13:01:31 ; Search time 10.8696 Seconds
(without alignments)
189.563 Million cell updates/sec

Title: US-09-801-784A-36

Perfect score: 50

Sequence: 1 PSAAVLTGSP 10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

at-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTREMBL 21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rviro:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	84.0	134	2	Q47122
2	42	84.0	167	2	Q93G69
3	40	80.0	170	2	Q93V20
4	40	80.0	433	13	Q9DE24
5	38	76.0	114	12	Q41238
6	38	76.0	114	12	Q41239
7	38	76.0	114	12	Q41240
8	38	76.0	114	12	Q41241
9	38	76.0	159	12	Q9YR11
10	38	76.0	233	12	Q91FU2
11	38	76.0	270	5	Q9NE74
12	38	76.0	579	12	Q9WJ53
13	38	76.0	579	12	Q86124
14	38	76.0	695	12	Q86123
15	38	76.0	2344	12	Q86117
16	38	76.0	2344	12	Q86119

17	37	74.0	534	2	Q9ANK2	Q9ank2 bradyrhizob
18	36	72.0	114	12	Q41209	Q41209 rabbit hemo
19	36	72.0	114	12	Q41210	Q41210 rabbit hemo
20	36	72.0	114	12	Q41211	Q41211 rabbit hemo
21	36	72.0	114	12	Q41212	Q41212 rabbit hemo
22	36	72.0	114	12	Q41213	Q41213 rabbit hemo
23	36	72.0	114	12	Q41214	Q41214 rabbit hemo
24	36	72.0	114	12	Q41215	Q41215 rabbit hemo
25	36	72.0	114	12	Q41218	Q41218 rabbit hemo
26	36	72.0	114	12	Q41219	Q41219 rabbit hemo
27	36	72.0	114	12	Q41220	Q41220 rabbit hemo
28	36	72.0	114	12	Q41221	Q41221 rabbit hemo
29	36	72.0	114	12	Q41222	Q41222 rabbit hemo
30	36	72.0	114	12	Q41223	Q41223 rabbit hemo
31	36	72.0	114	12	Q41226	Q41226 rabbit hemo
32	36	72.0	114	12	Q41229	Q41229 rabbit hemo
33	36	72.0	114	12	Q41231	Q41231 rabbit hemo
34	36	72.0	114	12	Q41232	Q41232 rabbit hemo
35	36	72.0	114	12	Q41234	Q41234 rabbit hemo
36	36	72.0	114	12	Q41237	Q41237 rabbit hemo
37	36	72.0	114	12	Q41242	Q41242 rabbit hemo
38	36	72.0	155	2	Q9ZAT3	Q9zat3 streptococc
39	36	72.0	233	12	Q91FU3	Q91fu3 porcine cir
40	36	72.0	342	16	Q99Y46	Q99y46 streptococc
41	36	72.0	427	3	Q74498	Q74498 schizosacch
42	36	72.0	537	3	Q02466	Q02466 schizosphy11
43	36	72.0	579	12	Q91ZJ8	Q91zj8 rabbit hemo
44	36	72.0	579	12	Q9YND3	Q9ynd3 rabbit hemo
45	36	72.0	579	12	Q91HR6	Q91hr6 rabbit hemo

ALIGNMENTS

RESULT 1

Q47122 PRELIMINARY; PRT; 134 AA.

AC Q47122; 01-NOV-1996 (TREMblrel. 01, Created)

DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE CsfA protein (Fragment).

DE CSFA.

GN Escherichia coli.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=9B1373;

RA Gaastera W., Kusters J.G., Van Dijk L.,

RT "The major subunit gene for CsfA fimbriae is duplicated in the CSfA

RT fimbrial operon."

RT Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; X97493; CAA66124.1; -

FT NON_TER 1 134

FT NON_TER 1 134

FT NON_TER 1 134

SQ SEQUENCE 134 AA; 13916 MW; 3EEFFDC5861396A4 CRC64;

Query Match 84.0%; Score 42; DB 2; Length 134;

Best Local Similarity 80.0%; Pred. No. 0.72;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSAAVLTGSP 10

DB 16 PTAVELTYSR 25

RESULT 2

Q93G69 PRELIMINARY; PRT; 167 AA.

ID Q93G69; 01-DEC-2001 (TREMblrel. 19, Created)

```
DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE CS4 major fimbriae subunit CsaB.
GN CSAB.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E11881A.
RA Altbaum Z.D., Levine M.M., Galen J.E., Barry E.M.;
RT "Isolation and characterization of ETEC CS4 fimbriae encoding genes,
RT and their expression in Shigella flexneri 2a guABA strain CVD 1204.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF296132; AAK97135.1; -.
SQ SEQUENCE 167 AA; 17344 MW; 94C77822A7C23A5A CRC64;

Query Match 84.0%; Score 42; DB 2; Length 167;
Best Local Similarity 80.0%; Pred. No. 0.92;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PSAVALTYSP 10
Db 49 PTAVELTYSP 58

RESULT 3
Q93V20
ID Q93V20 PRELIMINARY; PRT; 170 AA.
AC Q93V20;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE Colonization factor antigen 1.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Z., Li S., Huang C.;
RT "Sequence analysis of the colonization factor antigen 1 gene of ETEC
RT and observation of CFA/I recombinant clone with electron microscopy.";
RL Chin J. Biotechnol. 9:57-61(1993).
DR EMBL: S73191; AAB30543.1; -.
SQ SEQUENCE 170 AA; 17433 MW; 894347E2F43E5B34 CRC64;

Query Match 80.0%; Score 40; DB 2; Length 170;
Best Local Similarity 80.0%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PSAVALTYSP 10
Db 49 PSAVALTYSP 58

RESULT 4
Q9DE24
ID Q9DE24 PRELIMINARY; PRT; 433 AA.
AC Q9DE24;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE Forkhead transcription factor cl.2.
GN FOXCl.2.
OS Brachydanio rerio (Zebrafish) (Zebra daniel).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=21095190; PubMed=11165495;
RA Topczewska J.M., Topczewski J., Solnica-Krezel L., Hogan B.L.M.;
RT "Sequence and expression of zebrafish foxc1a and foxc1b, encoding
RT conserved forkhead/winged helix transcription factors.";
RL Mech. Dev. 100:343-347(2001).
DR EMBL: AF219950; AAG44242.1; -.
DR HSSP; Q63245; 2HPH.
DR InterPro; IPR001766; TF_Fork_head.
DR Pfam; PF00250; Fork head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS00039; FORK_HEAD_3; 1.
SQ SEQUENCE 433 AA; 47518 MW; 8941A9DBB9B837B9 CRC64;

Query Match 80.0%; Score 40; DB 13; Length 433;
Best Local Similarity 70.0%; Pred. No. 7.2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PSAVALTYSP 10
Db 281 PGSVSLTYSP 290

RESULT 5
O41238
ID O41238 PRELIMINARY; PRT; 114 AA.
AC O41238;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, last annotation update)
DE Capsid protein (Fragment).
OS Rabbit hemorrhagic disease virus (RHDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Lagovirus.
OX NCBI_TaxID=11976;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPAIN 90;
RX MEDLINE=97314153; PubMed=9170495;
RA Nowotny N., Bascunana C.R., Ballagi-Pordany A., Gavrier-Widen D.,
RA Uhlen M., Belak S.;
RT "Phylogenetic analysis of rabbit haemorrhagic disease and European
RT brown hare syndrome viruses by comparison of sequences from the capsid
RT protein gene.";
RL Arch. Virol. 142:657-673(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPAIN 90;
RA Ros C.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U65346; AAB62790.1; -.
DR InterPro; IPR004005; Calici_coat.
DR Pfam; PF00915; Calici_coat; 1.
FT NON_TER 1
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 11238 MW; 72BD37F898E99E0A CRC64;

Query Match 76.0%; Score 38; DB 12; Length 114;
Best Local Similarity 70.0%; Pred. No. 4;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PSAVALTYSP 10
Db 51 PSANAITYP 60

RESULT 6
O41239
ID O41239 PRELIMINARY; PRT; 114 AA.
```

AC 041239;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DE 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Capsid protein (Fragment).
 OS Rabbit hemorrhagic disease virus (RHDV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Lagovirus.
 NCBI_TaxID=11976;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPAIN 95A;
 RX MEDLINE=97314153; PubMed=9170495;
 RA Nowotny N., Basconana C.R., Ballagi-Pordany A., Gavler-Widen D.,
 RA Uhlen M., Belak S.;
 RT "Phylogenetic analysis of rabbit haemorrhagic disease and European
 RT brown hare syndrome viruses by comparison of sequences from the capsid
 RT protein gene."
 RL Arch. Virol. 142:657-673(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPAIN 95A;
 RA Ros C.;
 RI Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RI EMBL; U65347; AAB62791.1; .
 RI InterPro; IPR004005; Calici_coat.
 RI Pfam; PF00915; Calici_coat; 1.
 FT NON_TER 1 114
 FT SEQUENCE 114 AA; 11234 MW; B117E02F5A277BF CRC64;
 SQ

Query Match 76.0%; Score 38; DB 12; Length 114;
 Best Local Similarity 70.0%; Pred. No. 4;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 PSVAULTYSP 10
 DB 51 PSNAATYTP 60

RESULT 7
 ID 041240 PRELIMINARY; PRT; 114 AA.
 AC 041240;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Capsid protein (Fragment).
 OS Rabbit hemorrhagic disease virus (RHDV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Lagovirus.
 NCBI_TaxID=11976;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPAIN 95B;
 RX MEDLINE=97314153; PubMed=9170495;
 RA Nowotny N., Basconana C.R., Ballagi-Pordany A., Gavler-Widen D.,
 RA Uhlen M., Belak S.;
 RT "Phylogenetic analysis of rabbit haemorrhagic disease and European
 RT brown hare syndrome viruses by comparison of sequences from the capsid
 RT protein gene."
 RL Arch. Virol. 142:657-673(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPAIN 95B;
 RA Ros C.;
 RI Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RI EMBL; U65348; AAB62792.1; .
 RI InterPro; IPR004005; Calici_coat.
 RI Pfam; PF00915; Calici_coat; 1.
 FT NON_TER 1 114
 FT SEQUENCE 114 AA; 11222 MW; 1F109F7C05BBA3 CRC64;
 SQ

Query Match 76.0%; Score 38; DB 12; Length 114;
 Best Local Similarity 70.0%; Pred. No. 4;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 PSVAULTYSP 10
 DB 51 PSNAATYTP 60

RESULT 8
 ID 041241 PRELIMINARY; PRT; 114 AA.
 AC 041241;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DE 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Capsid protein (Fragment).
 OS Rabbit hemorrhagic disease virus (RHDV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Lagovirus.
 NCBI_TaxID=11976;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPAIN 95C;
 RX MEDLINE=97314153; PubMed=9170495;
 RA Nowotny N., Basconana C.R., Ballagi-Pordany A., Gavler-Widen D.,
 RA Uhlen M., Belak S.;
 RT "Phylogenetic analysis of rabbit haemorrhagic disease and European
 RT brown hare syndrome viruses by comparison of sequences from the capsid
 RT protein gene."
 RL Arch. Virol. 142:657-673(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPAIN 95C;
 RA Ros C.;
 RI Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RI EMBL; U65349; AAB62793.1; .
 RI InterPro; IPR004005; Calici_coat.
 RI Pfam; PF00915; Calici_coat; 1.
 FT NON_TER 1 114
 FT SEQUENCE 114 AA; 11220 MW; 2925FD2965BC98A1 CRC64;
 SQ

Query Match 76.0%; Score 38; DB 12; Length 114;
 Best Local Similarity 70.0%; Pred. No. 4;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 PSVAULTYSP 10
 DB 51 PSNAATYTP 60

RESULT 9
 ID 09YR11 PRELIMINARY; PRT; 159 AA.
 AC 09YR11;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ORF-2.
 OS porcine circovirus type 2-C.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 NCBI_TaxID=85543;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20142849; PubMed=10680656;
 RA Hamel A.L., Lin L.L., Sachvie C., Grudski E., Nayar G.P.S.;
 RT "PCR detection and characterization of type-2 porcine circovirus."
 RL Can. J. Vet. Res. 64:44-52(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hamel A.L., Nayar G.P.S.;

RT "Nucleotide sequence of four different isolates of circovirus detected
RT in pigs with various clinical syndromes.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF109398; AAD03062.1; -;
DR InterPro; IPR003383; Circo_ORF2.
DR Pfam; PF02443; Circo_ORF2; 1.
SQ SEQUENCE 159 AA; 19006 MW; E457711A26B560DB CRC64;

Query Match 76.0%; Score 38; DB 12; Length 159;
Best Local Similarity 70.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PSAVALTYSP 10
DB 131 PKATALTYDP 140

RESULT 10
QY1FU2 PRELIMINARY; PRT; 233 AA.
AC Q91FU2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Putative capsid protein.
GN CAP.
OS porcine circovirus type 2.
OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
OX NCBI_TaxID=85708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26607;
RX MEDLINE=20341537; PubMed=10878032;
RA Fenaux M., Halbur P.G., Gill M., Toth T.E., Meng X.J.;
RT "Genetic characterization of type-2 porcine circovirus (PCV-2) from
RT pigs with PMS in different geographic regions of North America and
RT development of a differential PCR-RFLP assay to detect and
RT differentiate infections between PCV-1 and PCV-2.";
RL J. Clin. Microbiol. 38:2494-2503(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=26607;
RA Fenaux M., Halbur P.G., Gill M., Toth T.E., Meng X.J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF264039; AAF87229.1; -;
DR InterPro; IPR003383; Circo_ORF2.
DR Pfam; PF02443; Circo_ORF2; 1.
SQ SEQUENCE 233 AA; 27965 MW; 1482D8D2871E76F3 CRC64;

Query Match 76.0%; Score 38; DB 12; Length 233;
Best Local Similarity 70.0%; Pred. No. 9.1;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PSAVALTYSP 10
DB 131 PKATALTYDP 140

RESULT 11
QYNE74 PRELIMINARY; PRT; 270 AA.
AC Q9NE74;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Hypothetical 29.3 kDa protein.
GN L5075.02;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;

RA Beck A., Klages S., Reinhardt R., Ivens A.C., Quail M.,
RA Rajandream M.A., Barrell B.G.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL163552; CAB86964.1; -;
KW Hypothetical protein.
SQ SEQUENCE 270 AA; 29335 MW; 5B91DA37A16FC3CB CRC64;

Query Match 76.0%; Score 38; DB 5; Length 270;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PSAVALTYSP 10
DB 132 PSAVALEYLP 141

RESULT 12
Q9WJS3 PRELIMINARY; PRT; 579 AA.
ID Q9WJS3
AC Q9WJS3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Capsid structural protein VP60.
GN VP60.
OS Rabbit hemorrhagic disease virus (RHDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Lagovirus.
OX NCBI_TaxID=11976;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BIENHUTTENSTADT;
RA Schirmeier H., Reimann I., Koellner B.;
RT "Pathogenic, antigenic and molecular properties of rabbit haemorrhagic
RT disease virus (RHDV) isolated from vaccinated rabbits: Detection and
RT preliminary characterization of antigenic variants.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y15440; CAA75631.1; -;
DR InterPro; IPR004005; Calici_coat.
DR Pfam; PF00915; Calici_coat; 1.
SQ SEQUENCE 579 AA; 60262 MW; 7264E5FF1BD6288B CRC64;

Query Match 76.0%; Score 38; DB 12; Length 579;
Best Local Similarity 70.0%; Pred. No. 26;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSAVALTYSP 10
DB 429 PSANAITYP 438

RESULT 13
Q86124 PRELIMINARY; PRT; 579 AA.
ID Q86124
AC Q86124;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE VP60.
OS Rabbit hemorrhagic disease virus (RHDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Lagovirus.
OX NCBI_TaxID=11976;
RN [1]
RP SEQUENCE FROM N.A.

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RX STRAIN=AST/89;
RX MEDLINE=94358742; PubMed=80779941;
RA Boga U., Casais R., Marin M., Martin-Alonso J., Carmenes R.,
RA Parra F.;
RT "Molecular cloning, sequence and expression of the capsid protein gene
RT from rabbit hemorrhagic disease virus (Spanish isolate AST/89).";
RL J. Gen. Virol. 75:2409-2413(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=AST/89;
RX MEDLINE=93070565; PubMed=1441736;
RA Boga U., Marin M., Casais R., Prieto M., Parra F.;
RT "IN VITRO TRANSLATION OF A SUBGENOMIC mRNA FROM PURIFIED VIRIONS OF
RT THE SPANISH FIELD ISOLATE AST/89 OF RABBIT HEMORRHAGIC DISEASE VIRUS
RT (RHDV).";
RL Virus Res. 26:33-40(1992).
RN [3]
RN SEQUENCE OF 1-32 FROM N.A.
RC STRAIN=AST/89;
RX MEDLINE=93255896; PubMed=80488721;
RA Parra F., Boga U.A., Marin M.S., Casais R.;
RT "The amino terminal sequence of VP60 from rabbit hemorrhagic disease
RT virus supports its putative subgenomic origin.";
RL Virus Res. 27:219-228(1993).
RN [4]
RN SEQUENCE FROM N.A.
RC STRAIN=AST/89;
RA Parra F.;
RL Submitted (JUL-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z24577; CAA80883.1; -.
DR InterPro; IPR004005; Calici_coat.
DR Pfam; PF00915; Calici_coat; 1.
SQ SEQUENCE 579 AA; 60195 MW; 0806D11DA062165A CRC64;

Query March 76.0%; Score 38; DB 12; Length 579;
Best Local Similarity 70.0%; Pred. No. 26;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps

QY 1 PSAAVATYSP 10
|||::||:|
Db 429 PSANATYTP 438

RESULT 14
Q86123 PRELIMINARY; PRT; 695 AA.
ID 086123 AC 086123;
DT 01-NOV-1996 (TRMBLrel. 01, Created)
DT 01-NOV-1996 (TRMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)
DE ORF1 protein (Fragment).
OS Rabbit hemorrhagic disease virus (RHDV).
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
Lagovirus.
NCBI_TaxID=11976;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=AST/89;
RX MEDLINE=94358742; PubMed=80779941;
RA Boga U., Casais R., Marin M., Martin-Alonso J., Carmenes R.,
RA Prieto M., Parra F.;
RT "Molecular cloning, sequence and expression of the capsid protein gene
RT from rabbit hemorrhagic disease virus (Spanish isolate AST/89).";
RL J. Gen. Virol. 75:2409-2413(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=AST/89;
RX MEDLINE=93070565; PubMed=1441736;
RA Boga U., Marin M., Casais R., Prieto M., Parra F.;
RT "IN VITRO TRANSLATION OF A SUBGENOMIC mRNA FROM PURIFIED VIRIONS OF
RT THE SPANISH FIELD ISOLATE AST/89 OF RABBIT HEMORRHAGIC DISEASE VIRUS
RT (RHDV).";
RL Virus Res. 26:33-40(1992).

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RN      [3]
RP      SEQUENCE OF 1-149 FROM N.A.
RC      STRAIN=AST/89;
RX      MEDLINE=93255896; PubMed=8488721;
RA      Parra F., Boga J.A., Marin M.S., Casais R.;
RT      "The amino terminal sequence of VP60 from rabbit hemorrhagic disease
RL      virus supports its putative subgenomic origin.";
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=AST/89;
RA      Parra F.;
RL      Submitted (JUL-1993) to the EMBL/GenBank/DBJ databases.
DR      EMBL; Z24757; CAAB0881.1; -.
DR      InterPro; IPR004005; Calici_coat.
DR      InterPro; IPR004004; Calici_pol_hel.
DR      Pfam; PF00915; Calici_coat; 1.
DR      PRINTS; PR00918; CALICIVIRUSNS.
RN      FT
RP      NON TER
RL      1
SQ      SEQUENCE 695 AA; 73731 MW; C2D92162B99A989A CRC64;

Query Match      76.0%; Score 36; DB 12; Length 695;
Best Local Similarity 70.0%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      1 PSAVALTYSP 10
      ||| |::|:|
DB      545 PSAVALITYTP 554

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	RESULT	15			
ID	Q86117		PRELIMINARY;	PRT:	2344 AA.
AC	Q86117;				
DT	01-NOV-1996	(TREMBLrel_01,	Created)		
DT	01-NOV-1996	(TREMBLrel_01,	Last sequence update)		
DT	01-JUN-2002	(TREMBLrel_21,	Last annotation update)		
DE	(SD) complete genomic RNA.				
OS	Rabbit hemorrhagic disease virus (RHDV).				
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;				
OX	Lagovirus.				
NCBI_TaxId=11976;					
RM	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=SD.				
RX	MEDLINE=95250304; PubMed=7732658;				
RA	Raeschner D., Huguet S., Madelaine M.F., Vautherot J.F. ;				
RT	"Sequence and genome organization of a rabbit haemorrhagic disease				
RL	virus isolate from a wild rabbit.";				
VL	Virus Genes 9:121-132(1995).				
DR	EMBL, Z29514; CAA82635.1; .				
DR	InterPro: IPR004005; Calici_coat.				
DR	InterPro: IPR004004; Calici_pol_hel.				
DR	InterPro: IPR000317; Endoplas_C24.				
DR	InterPro: IPR000605; RNA_helicase.				
DR	InterPro: IPR001205; RNA_pol_P3D.				
DR	pfam; PF00915; calici_coat_1.				
DR	pfam; PF03510; peptidase_C24; 1.				
DR	pfam; PF00680; RNA_dep_RNA_pol; 1.				
DR	pfam; PF00910; RNA_helicase; 1.				
DR	PRINTS; PR00916; 2CENDOPTASE.				
DR	PRINTS; PR00918; CALICIVIRUSNS.				
SO	SEQUENCE	2344 AA;	257121 NM;	193B1D447658BF77 CR664;	
Query Match		76.0%;	Score 38;	DB 12;	Length 2344;
Best Local Similarity		70.0%;	Pred. No. 1.3e+02;		
Matches	7;	Conservative	2;	Mismatches	1;
Gaps	0;				
Indels	0;				
1	PSAVALTYP	10			
DB	2194 PSANAITYP	2203			

RESULT 16

Q86119 AC Q86119 PRELIMINARY; PRT; 2344 AA.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Polyprotein.
GN P254.
OS Rabbit hemorrhagic disease virus (RHDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Lagovirus.
OX NCBI_TaxID=11976;
RN [1]
RP SEQUENCE OF 1649-2344 FROM N.A.
RC STRAIN AST/89;
RX MEDLINE=94358742; PubMed=8077941;
RA Boga J., Casais R., Marin M., Martin-Alonso J., Carnenes R.,
RA Prieto M., Parra F.;
RT "Molecular cloning, sequence and expression of the capsid protein gene
from rabbit hemorrhagic disease virus (Spanish isolate AST/89).";
RL J. Gen. Virol. 75:2409-2413(1994).
RN [2]
RP SEQUENCE OF 1649-1795 FROM N.A.
RC STRAIN AST/89;
RX MEDLINE=94255896; PubMed=8488721;
RA Parra F., Boga J.A., Marin M.S., Casais R.;
RT "The amino terminal sequence of VP60 from rabbit hemorrhagic disease
virus supports its putative subgenomic origin.";
RL Virus Res. 27:219-228(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN AST/89;
RA "Genomic organization of rabbit hemorrhagic disease virus determined
by direct amino acid sequence of the polyprotein processed products.";
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z49271; (AA89265.1);
DR MEROPS; C24.001; ;
DR InterPro; IPR004005; Calici coat.
DR InterPro; IPR004004; Calici pol. hel.
DR InterPro; IPR000317; Endoptase C24.
DR InterPro; IPR000605; RNA_helicase.
DR InterPro; IPR001205; RNA_pol. p3d.
DR Pfam; PF00915; Calici coat; 1.
DR Pfam; PF03510; Peptidase C24; 1.
DR Pfam; PF05680; RNA dep. RNA pol. 1.
DR Pfam; PF05910; RNA_helicase; 1.
DR PRINTS; PR00916; 2CENDOPTASE.
DR PRINTS; PR00918; CALICIVIRUS.
SQ SEQUENCE 2344 AA; 256769 MW; 9264ADA9E6A49D64 CRC64;

Query Match 76.0%; Score 38; DB 12; Length 2344;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSAAVITYSP 10
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Db 2194 PSAAVITYTP 2203
| | | | |

RESULT 17

Q9ANK2 AC Q9ANK2 PRELIMINARY; PRT; 534 AA.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ID156.
GN ID156.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Bradyrhizobium.

OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=110SPC4;
RX MEDLINE=21101824; PubMed=11157954;
RA Gottfert M., Rothlisberger S., Kundig C., Beck C., Marty R.,
RA Hennecke H.;
RT "Potential symbiosis-specific genes uncovered by sequencing a 410-kb
DNA region of the Bradyrhizobium japonicum chromosome.";
RL J. Bacteriol. 183:1405-1412(2001).
DR EMBL; AF322012; AAG60768.1; ;
DR InterPro; IPR004291; Transposase 25.
DR Pfam; PF03050; Transposase 25; 1.
SQ SEQUENCE 534 AA; 59482 MW; 54C2B194E6EFC4D CRC64;

Query Match 74.0%; Score 37; DB 2; Length 534;
Best Local Similarity 70.0%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PSAAVITYSP 10
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Db 294 PPAVAYTYAP 303
| | | | |

RESULT 18

Q41209 AC Q41209 PRELIMINARY; PRT; 114 AA.
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Capsid protein (Fragment).
OS Rabbit hemorrhagic disease virus (RHDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Lagovirus.
OX NCBI_TaxID=11976;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AUSTRIA 89B;
RX MEDLINE=97314153; PubMed=9170495;
RA Nowotny N., Bascunana C.R., Ballagi-Pordany A., Gavriel-Widen D.,
RA Uhlen M., Belak S.;
RT "Phylogenetic analysis of rabbit haemorrhagic disease and European
brown hare syndrome viruses by comparison of sequences from the capsid
protein gene.";
RL Arch. Virol. 142:657-673(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AUSTRIA 89B;
RA Ros C.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U65317; AAB62761.1; ;
DR InterPro; IPR004005; Calici coat.
DR Pfam; PF00915; Calici coat; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 11206 MW; 952481847E9AF19B CRC64;

Query Match 72.0%; Score 36; DB 12; Length 114;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSAAVITYSP 10
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Db 51 PNASAITYP 60
| | | | |

RESULT 19

Q41210 AC Q41210 PRELIMINARY; PRT; 114 AA.
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
 DE Capsid protein (Fragment).
 OS Rabbit hemorrhagic disease virus (RHDV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Lagovirus.
 NCBI_TaxID=11976;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=AUSTRIA 90;
 RX MEDLINE=97314153; PubMed=9170495;
 RA Nowotny N., Bascunana C.R., Ballagi-Pordany A., Gavier-Widen D.,
 Uhlen M., Belak S.;
 RT "Phylogenetic analysis of rabbit haemorrhagic disease and European
 brown hare syndrome viruses by comparison of sequences from the capsid
 protein gene."
 RT Arch. Virol. 142:657-673(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AUSTRIA 90;
 RA Ros C.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U65318; AAB62762.1; Calici_coat.
 DR InterPro; IPR004005; Calici_coat.
 DR Pfam; PF00915; Calici_coat; 1.
 FT NON_TER 1 1
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 11236 MW; 8E2531847E9AF19B CRC64;
 QY 1 PSAVALTYSP 10
 Db 51 PNASAITYP 60
 RESULT 20
 ID 041211 PRELIMINARY; PRT; 114 AA.
 AC 041211;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
 DE Capsid protein (Fragment).
 OS Rabbit hemorrhagic disease virus (RHDV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Lagovirus.
 NCBI_TaxID=11976;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=AUSTRIA 91A;
 RX MEDLINE=97314153; PubMed=9170495;
 RA Nowotny N., Bascunana C.R., Ballagi-Pordany A., Gavier-Widen D.,
 Uhlen M., Belak S.;
 RT "Phylogenetic analysis of rabbit haemorrhagic disease and European
 brown hare syndrome viruses by comparison of sequences from the capsid
 protein gene."
 RT Arch. Virol. 142:657-673(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AUSTRIA 91A;
 RA Ros C.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U65319; AAB62763.1; Calici_coat.
 DR InterPro; IPR004005; Calici_coat.
 DR Pfam; PF00915; Calici_coat; 1.
 FT NON_TER 1 1
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 11236 MW; 8E2531847E9AF19B CRC64;
 QY 1 PSAVALTYSP 10
 Db 51 PNASAITYP 60
 Query Match 72.0%; Score 36; DB 12; Length 114;
 Best Local Similarity 60.0%; Pred. No. 10;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PSAVALTYSP 10
 Db 51 PNASAITYP 60
 RESULT 21
 ID 041212 PRELIMINARY; PRT; 114 AA.
 AC 041212;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
 DE Capsid protein (Fragment).
 OS Rabbit hemorrhagic disease virus (RHDV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Lagovirus.
 NCBI_TaxID=11976;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=AUSTRIA 91B;
 RX MEDLINE=97314153; PubMed=9170495;
 RA Nowotny N., Bascunana C.R., Ballagi-Pordany A., Gavier-Widen D.,
 Uhlen M., Belak S.;
 RT "Phylogenetic analysis of rabbit haemorrhagic disease and European
 brown hare syndrome viruses by comparison of sequences from the capsid
 protein gene."
 RT Arch. Virol. 142:657-673(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AUSTRIA 91B;
 RA Ros C.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U65320; AAB62764.1; Calici_coat.
 DR InterPro; IPR004005; Calici_coat.
 DR Pfam; PF00915; Calici_coat; 1.
 FT NON_TER 1 1
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 11295 MW; 953F802F76A0419B CRC64;
 QY 1 PSAVALTYSP 10
 Db 51 PNASAITYP 60
 Query Match 72.0%; Score 36; DB 12; Length 114;
 Best Local Similarity 60.0%; Pred. No. 10;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PSAVALTYSP 10
 Db 51 PNASAITYP 60
 RESULT 22
 ID 041213 PRELIMINARY; PRT; 114 AA.
 AC 041213;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
 DE Capsid protein (Fragment).
 OS Rabbit hemorrhagic disease virus (RHDV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Lagovirus.
 NCBI_TaxID=11976;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=AUSTRIA 93A;
 RX MEDLINE=97314153; PubMed=9170495;
 RA Nowotny N., Bascunana C.R., Ballagi-Pordany A., Gavier-Widen D.,
 Uhlen M., Belak S.;
 RT "Phylogenetic analysis of rabbit haemorrhagic disease and European
 brown hare syndrome viruses by comparison of sequences from the capsid
 protein gene."
 RT Arch. Virol. 142:657-673(1997).
 RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN AUSTRIA 93A;
RA Ros C.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U65321; AAB62765.1; -.
DR InterPro: IPR004005; Calici_coat.
DR Pfam: PF00915; Calici_coat; 1.
FT NON TER 1
FT NON TER 114
SQ SEQUENCE 114 AA; 11281 MW; 1AC6396F8D90EE99 CRC64;

Query Match 72.0%; Score 36; DB 12; Length 114;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSVAULTYSP 10
Db 51 PNASAITYTP 60

RESULT 23
O41214 PRELIMINARY; PRT; 114 AA.
AC O41214;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Capsid protein (Fragment).
OS Rabbit haemorrhagic disease virus (RHDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Lagovirus.
OX NCBI_TaxID=11976;
RN [1]
RP SEQUENCE FROM N.A.
RA Ros C.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U65322; AAB62766.1; -.
DR InterPro: IPR004005; Calici_coat.
DR Pfam: PF00915; Calici_coat; 1.
FT NON TER 1
FT NON TER 114
SQ SEQUENCE 114 AA; 11281 MW; 1AC6396F8D90EE99 CRC64;

Query Match 72.0%; Score 36; DB 12; Length 114;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSVAULTYSP 10
Db 51 PNASAITYTP 60

RESULT 24
O41215 PRELIMINARY; PRT; 114 AA.
AC O41215;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Capsid protein (Fragment).
OS Rabbit haemorrhagic disease virus (RHDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;

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OC Lagovirus.
OX NCBI_TaxID=11976;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AUSTRIA 93C;
RX MEDLINE=97314153; PubMed=9170495;
RA Nowotny N., Bascunana C.R., Ballagi-Pordany A., Gavier-Widen D.,
  Uhlen M., Belak S.;
RT "Phylogenetic analysis of rabbit haemorrhagic disease and European
  brown hare syndrome viruses by comparison of sequences from the capsid
  protein gene.";
RL Arch. Virol. 142:657-673(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AUSTRIA 93C;
RA Ros C.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U65323; AAB62767.1; -.
DR InterPro: IPR004005; Calici_coat.
DR Pfam: PF00915; Calici_coat; 1.
FT NON TER 1
FT NON TER 114
SQ SEQUENCE 114 AA; 11222 MW; 8AFACAA0A161D19B CRC64;

Query Match 72.0%; Score 36; DB 12; Length 114;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSVAULTYSP 10
Db 51 PNASAITYTP 60

RESULT 25
O41218 PRELIMINARY; PRT; 114 AA.
ID O41218;
AC O41218;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Capsid protein (Fragment).
OS Rabbit haemorrhagic disease virus (RHDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Lagovirus.
OX NCBI_TaxID=11976;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BELGIUM 90;
RX MEDLINE=97314153; PubMed=9170495;
RA Nowotny N., Bascunana C.R., Ballagi-Pordany A., Gavier-Widen D.,
  Uhlen M., Belak S.;
RT "Phylogenetic analysis of rabbit haemorrhagic disease and European
  brown hare syndrome viruses by comparison of sequences from the capsid
  protein gene.";
RL Arch. Virol. 142:657-673(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BELGIUM 90;
RA Ros C.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U65326; AAB62770.1; -.
DR InterPro: IPR004005; Calici_coat.
DR Pfam: PF00915; Calici_coat; 1.
FT NON TER 1
FT NON TER 114
SQ SEQUENCE 114 AA; 11222 MW; 4D253196FC0AE319 CRC64;

Query Match 72.0%; Score 36; DB 12; Length 114;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSVAULTYSP 10
Db 51 PNASAITYTP 60

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Db 51 PNASAITVTP 60

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Job time : 11.8696 secs
